09/752,292

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# WEST Search History

DATE: Saturday, June 08, 2002

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| *DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR* | | | |
| L6 | L1 same support | 47 | L6 |
| L5 | L4 not L3 | 18 | L5 |
| L4 | L1 same tag | 18 | L4 |
| L3 | L1 same capture | 7 | L3 |
| L2 | L1 same array | 12 | L2 |
| L1 | universal with (oligonucleotide or polynucleotide) | 650 | L1 |

END OF SEARCH HISTORY

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L2: Entry 3 of 12 File: PGPB Jan 31, 2002

DOCUMENT-IDENTIFIER: US 20020012926 A1
TITLE: Combinatorial array for nucleic acid analysis

Summary of Invention Paragraph (2):
[0003] This invention relates in general to an array, including a universal array, for the analysis of nucleic acids, such as DNA. The devices and methods of the invention can be used for identifying gene expression patterns in any organism. More specifically, the universal arrays of the invention comprise oligonucleotide probes of all possible oligonucleotide sequences having a specified length n that may be selected by a user. The invention also relates to analytical methods which can be used to analyze data (e.g., hybridization data) from such arrays.

Summary of Invention Paragraph (17):
[0018] A further object of the invention is to provide a universal micro-array; i.e., an array of oligonucleotides having a specified sequence length n (referred to herein as "n-mers") wherein all possible nucleotide sequence of length n are present on the array. Current technologies use chips having only certain specific oligonucleotides that are carefully selected to detect particular genes. Thus, for every organism (or even for different cells from the same organism that express different genes) it is necessary to design a new micro-array. The universal arrays of this invention therefore offer the advantage of being useful for studying gene expression in any cell or organism; thereby making a specially designed chip unnecessary.

Summary of Invention Paragraph (18):
[0019] Still another object of the invention is to determine and provide useful values for the oligonucleotide sequence length n that may be used in a universal array, particularly for preferred embodiments of analyzing gene expression.

Summary of Invention Paragraph (23):
[0024] The invention is based in part on the inventors' discovery that appropriate probe lengths n may be selected that are small enough that fabrication of universal micr-arrays comprising all oligonucleotide probe sequence of length n is feasible and average probe "degeneracy" is low (i.e., each probe only hybridizes to, on average, only a few nucleic acids or genes). As a result, a hybridization matrix describing the "mapping" of expression levels to hybridization data in an experiment may be easily deconvoluted using the algorithms of the invention to identify relatively small subblocks.

Detail Description Paragraph (50):
[0084] The universal array of the present invention consists of a regular pattern of distinct spots of DNA sequences, each spot containing oligonucleotide strands of length n. In the set

Detail Description Paragraph (132):
[0162] It is noted that the methods of the invention are not limited to the particular mismatch model described above and that other models, which will be readily apparent to the skilled artisan, may also be used. For exdample, a variety of thermodynamic models for nucleic hybridization are well known in the art [1, 6, 8, 14, 18]. Using such models, a skilled artisan may readily determine (e.g, by calculation) a number of sequences c(n) of length n that will hybridize or are capable of hybridizing to an oligonucleotide probe of length n. Thus, for a given collection of No different oligonucleotide probes having a particular sequence length n (for example, a collection of N.sub.0=4.sup.n probes on a universal array) the number of sequences <c(n)> that may hybridize, on average, to a given probe can be readily calculated or otherwise determined. The probability of binding is expected to increase by this factor so that

the average probe degeneracy may be provided by the relation 9 d ( n ) = N g N 0 ( 1 - n + L ) .times. c ( n )

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L5: Entry 5 of 18 File: USPT Jul 18, 2000

DOCUMENT-IDENTIFIER: US 6090549 A
TITLE: Use of continuous/contiguous stacking hybridization as a diagnostic tool

Detailed Description Paragraph Right (15):
In addition to the use of universal base or four-base approach, different mobile oligonucleotides, among the 1024 possibilities in the case of a pentamer mobile fraction, can be labeled with different fluorochromes. In the case of two different labels, the number of hybridizations will decrease by a factor of two. In the case of four different labels, the number of required hybridizations will decrease by a factor of four. This use of different labels is illustrated in FIGS. 2 and 3 whereby the geometric shapes of a circle, triangle, pentagon and square graphically represent different tags or fluorochromes.